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INBREEDING DEPRESSION OF CAPTIVE MALAYAN GAUR (*Bos gaurus hubbacki*) AT JENDERAK SELATAN WILDLIFE CONSERVATION CENTRE, PAHANG

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The Malayan gaur or locally known as Seladang (*Bos gaurus hubbacki*) is the second largest terrestrial mammal in Malaysia. In Peninsular Malaysia, wild gaur can be found in considerable numbers in states of Perak, Pahang and Terengganu (Muhamad Rizal, pers. comm.). According to Conry (1981), the home range of Malayan gaur differ with sex and age. Conry (1981) calculated the home range of a herd in Lepar River Valley (central Pahang) and he found that adult male have an estimated home range of 7,018 ha, adult female with 5,213 ha, and yearling male had a home range of 2,989 ha. Gaur food preference was affected by elevation from sea level (increase in elevation limit choice of food) and types of habitat (i.e. primary forest, secondary forest, agricultural area) within their home range (Ebil, 1982, 2009). Gaur preferred 17 species of shrubs and six species of grasses (Ebil, 2009). According to Ebil (2009) the most preferred shrubs based on habitat are *Shorea acuminata* (primary forest)*, Melastoma malabathricum* (secondary forest)*, Erythrina variegata* (agricultural area) and as for grasses species, the gaur favour *Imperata cylindrica* (primary forest), *Paspalum conjugatum* (secondary forest), and *Paspalum vaginatum* (agricultural area).

The gaur is listed as vulnerable by the International Union for Conservation of Nature and Natural Resources (IUCN) Red List of Threatened Species (Duckworth *et al*., 2008) and is a totally protected species under the Wildlife Conservation Act 2010 [Act 716]. As part of gaur *ex-situ* conservation effort, the

Department of Wildlife and National Parks (DWNP) Peninsular Malaysia has established the Jenderak Selatan Wildlife Conservation Centre (JSWCC) in 1979 (GPS coordinate: 3°38’18”N 102°18’11”E) and the captive breeding programme began in 1982 with a pair of wild gaur as initial breeder (Sahir, 1999). In April 1985, the first gaur was born in captivity and was named Jenderak. Since then JSWCC have recorded birth of gaur every year and the latest was in November 2015 marking the 30 years since the first gaur was successfully born in captivity. Sahir (1999) noted that the captive breeding programme was successful and there was no inbreeding. Nonetheless, the current captive population is undoubtedly inbred as there is no new bloodline introduced since the programme began.

Inbreeding is defined as mating among relative with common ancestor (Paige, 2010). Theoretically, inbreeding will reduce fitness in the offspring produced by inbred mating and this may lead to inbreeding depression which decreases fecundity and increases susceptibility to disease and mortality (Lacy, 1997). Several studies have suggested that there is correlation between inbreeding depression and population declines of captive population (Frankham, 1995; Bijlsma *et al*., 2000) as well as extinction risk of wild population (Westemeier *et al*., 1998; Brook *et al*., 2002). The combined effect of deterministic (habitat loss, overexploitation, impact of introduced species, and pollution) and stochastic factors (demographic, genetic, environmental stochasticity, and natural catastrophe) can drive wildlife species to extinction (Lande *et al*, 2003; Frankham, 2010). A study by O’Grady *et al*. (2006) using stochastic computer models have found that extinction risk for most threatened mammals increased due to inbreeding depression and have suggested that it is very important to avoid inbreeding. To date there were no assessment being carried out to determine the rate of inbreeding on captive Malayan gaur in Peninsular Malaysia either using genetic marker or pedigree record. This paper aim to give an insight on what is the current level of inbreeding of the captive Malayan gaur at JSWCC.

For this study, data was obtained from the studbook of JSWCC which contained 160 records of gaur (86 females, 74 males) including six wild individuals caught between 1982 and 2001. Other individuals were born in captive between 1985 and 2015. The inbreeding coefficient (F) of each individual can be defined as “the probability that two homologous alleles in an individual are identical by descent (IBD)” (Hedrick, 2011). There are other reason for alleles to be identical but F only consider the mathematical probability that the alleles originate from a common ancestor. F can be estimated from the pedigree data using PEDIGREE

VIEWER (Szulkin & Sheldon, 2007; Walling *et al*., 2011) version 6.5f (Kinghorn & Kinghorn, 2015). Individuals with information of both parents and at least one grandparents were assigned to dataset labelled as N1. The dataset is restricted further as N2 to include only individuals with both parents and all four grandparents known. N1 and N2 were compared to see the effect of insufficient pedigree depth on frequency of inbreeding. Neonatal and first year survival are defined as binary trait. If the individual was known to have died within 28 days (neonate) or 365 days (first year) from its date of birth, it will be recorded as 0 and if it survived, 1 will be recorded. Individuals with higher inbreeding coefficient is expected to survive less. Mortality rate was calculated by number of dead individuals over total number of birth in a year.

Pedigree of captive Malayan gaur constructed from studbook data of JSWCC is shown in Figure 1 while Table 1 list the inbreeding coefficient of each gaur individual. Out of 160 individuals, 141 individual were assigned as N1. Out of it, 88 individuals (62.4%) had a pedigree-based inbreeding-coefficient (F) of greater than 0 with a mean F of 0.1048. Figure 2 shows the distribution of inbreeding coefficient (F) for individuals with F>0. When only considering individuals that have information of all four grandparents (N2), dataset were reduced to 87 records and surprisingly all 87 individuals (100%) have F of more than 0 with a mean F of 0.1898. This is similar to the result obtained by Walling *et al*. (2011), which suggest that insufficient pedigree depth underestimated the frequency of inbreeding. Nonetheless, the proportion of types of inbreeding event is similar between N1 and N2 (Table 2).

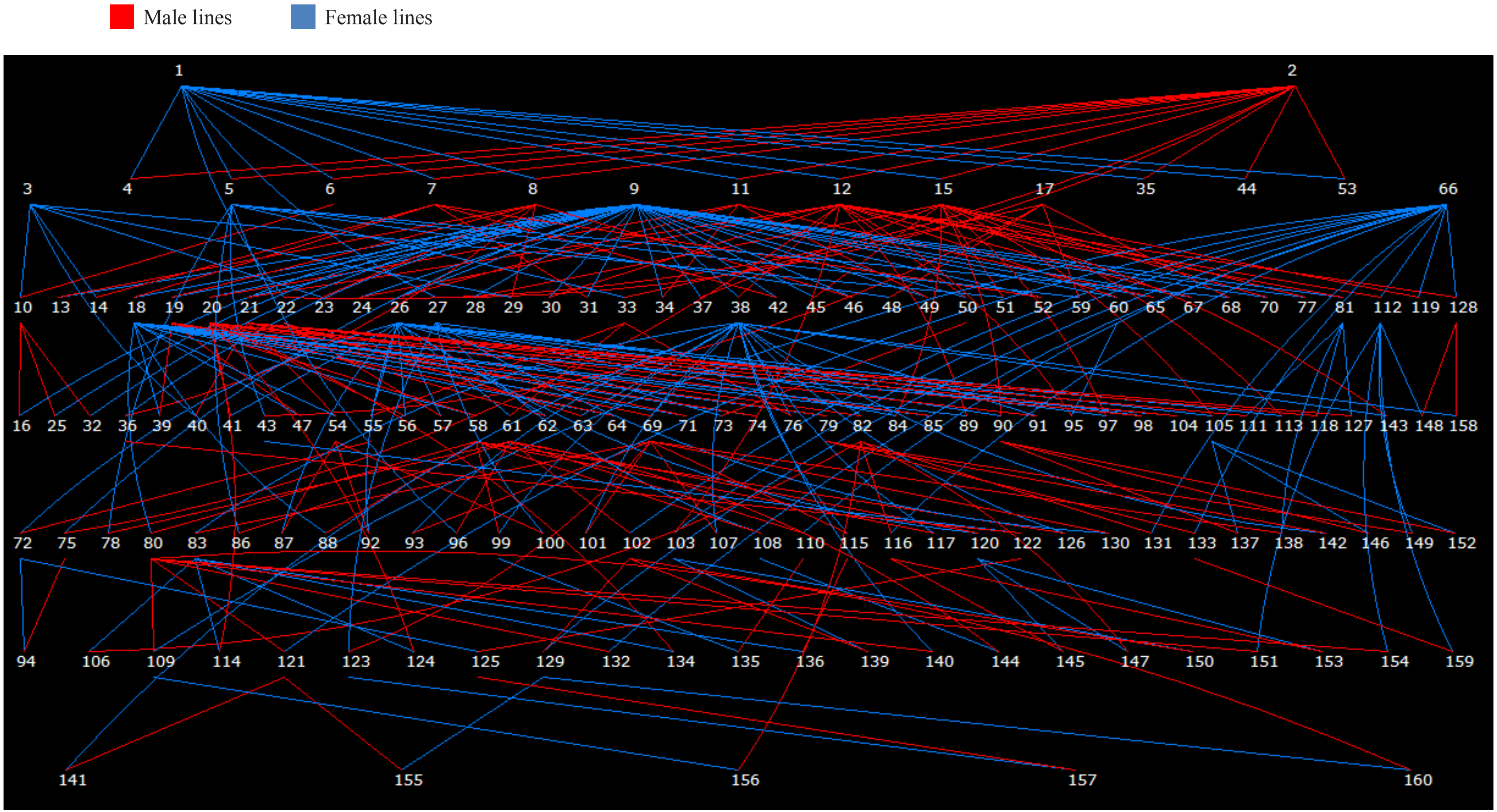

Figure 1 Pedigree of captive Malayan gaur constructed from studbook data of JSWCC using PEDIGREE VIEWER version 6.5f. Each gaur individuals are represented by number corresponding to Table 1. Inbreeding coefficient (F) of each individual are listed in Table 1 respectively.

Table 1 The inbreeding coefficient (F) of each gaur individual at JSWCC.

No.	NAME	F
1.	AHAD	0.0000
2.	BIAK	0.0000
3.	JADI	0.0000
4.	JENDERAK	0.0000
5.	SELATAN	0.0000
6.	JUN	0.0000
7.	OGY	0.0000
8.	MAS	0.0000
9.	MICHEAL	0.0000
10.	TINA	0.0000
11.	SEPT	0.0000
12.	NOVI	0.0000
13.	OS	0.0000
14.	KAN	0.0000
15.	JENA	0.0000
16.	TINI	0.0000
17.	MEK EDEN	0.0000
18.	BETA	0.0000
19.	MASDI	0.0000
20.	SEM	0.0000
21.	VIMIC	0.0000
22.	ROS	0.0000
23.	REDUP	0.0000
24.	NOMI	0.0000
25.	TIMI	0.0000
26.	AWANG	0.0000
27.	RUMPUN	0.0000
28.	KEMBANG	0.0000
29.	JIMI	0.0000
30.	DAMAK	0.0000
31.	MELOR	0.0000
32.	JANTAN	0.0000
33.	MAWAR	0.0000
34.	SABTU	0.0000
35.	BUNGA	0.0000
36.	AYU	0.0000
37.	CHERRY	0.0000
38.	CIKU	0.0000
39.	BADI	0.1875
40.	SELASIH	0.0000
41.	IPOH	0.2500
42.	ARANG	0.0000
43.	SUKOM	0.0000
44.	LABU	0.0000
45.	JAMBI	0.0000
46.	MELATI	0.0000
47.	BETI	0.1875
48.	SADEN	0.0000
49.	ATI	0.0000
50.	NONA	0.0000
51.	JENI	0.0000
52.	ONANG	0.0000
53.	SENJA	0.0000
54.	BEVI	0.1875
55.	WANGI	0.0625
56.	SAWI	0.2500
57.	SENA	0.1250
58.	TEH	0.1875
59.	UMI	0.0000
60.	NONI	0.0000
61.	POOJA	0.0625
62.	KHAN	0.2500
63.	NADI	0.1250
64.	JULY	0.1875
65.	MISEP	0.0000
66.	ISNIN	0.0000
67.	MICO	0.0000
68.	SELAT	0.0000
69.	CIWA	0.1875
70.	JIMA	0.0000
71.	DUMEX	0.1875
72.	IGAW	0.2813
73.	GAWI	0.1875
74.	BEMA	0.1875
75.	DIORA	0.0000
76.	CIRA	0.0625
77.	MIJA	0.0000
78.	SEPO	0.1875
79.	CINDA	0.1875
80.	BATEH	0.3438
81.	MINO	0.0000
82.	SEAKO	0.1875
83.	DIMA	0.3438
84.	VAKSIN	0.1250
85.	NAKITA	0.1875
86.	SEMPO	0.1875
87.	BAWANG	0.1875
88.	TEHBA	0.3438
89.	NOTA	0.1250
90.	AWANI	0.1250
91.	SENCUNI	0.1875
92.	AWAVI	0.1875
93.	KUCI	0.3438
94.	IXORA	0.1563
95.	ISNO	0.2500
96.	SEROJA	0.1875
97.	AWANA	0.1250
98.	SERUM	0.1250
99.	KUTEH	0.1875
100.	RUMBA	0.1250
101.	CICO	0.3438
102.	ISPO	0.0000
103.	NINO	0.0000
104.	VITA	0.1875
105.	WAJA	0.1250
106.	SEDI	0.3438
107.	CICI	0.3438
108.	PUTEH	0.1250
109.	BATIN	0.0000
110.	NIJA	0.0000
111.	MYVI	0.2500
112.	SAVVY	0.0000
113.	AVANZA	0.1250
114.	SEMMA	0.2656
115.	WAWA	0.3438
116.	SENI	0.0000
117.	CITEH	0.1875
118.	VINO	0.2500
119.	NINJA	0.0000
120.	ALZA	0.2813
121.	BATIS	0.0000
122.	MENDERANG	0.0625
123.	CIPUN	0.1250
124.	SEDIMA	0.2656
125.	GAWRANG	0.1328
126.	RAMADHAN	0.1875
127.	MIMIC	0.2500
128.	NOVIS	0.0000
129.	OPIS	0.2500
130.	RUCI	0.1250
131.	NIKO	0.0000
132.	BANIS	0.0000
133.	INDAH	0.0000
134.	MASEM	0.2656
135.	KUJA	0.0625
136.	WADI	0.4453
137.	WASATHIAH	0.3125
138.	CIMI	0.2188
139.	NOIS	0.1563
140.	TEHKU	0.1875
141.	CIKI	0.0938
142.	CICIN	0.1875
143.	CIVI	0.2500
144.	TEJA	0.1250
145.	NIZA	0.0898
146.	JANI	0.3125
147.	SEAZA	0.1797
148.	VIOS	0.2500
149.	DAVID	0.0625
150.	ISNON	0.1563
151.	SABA	0.0625
152.	AWAJA	0.3125
153.	ALNI	0.0898
154.	ARM	0.0625
155.	BATO	0.2031
156.	AKO	0.0938
157.	GAWRI	0.1387
158.	NOVCI	0.1250
159.	VYDA	0.1563
160.	TABIS	0.0313

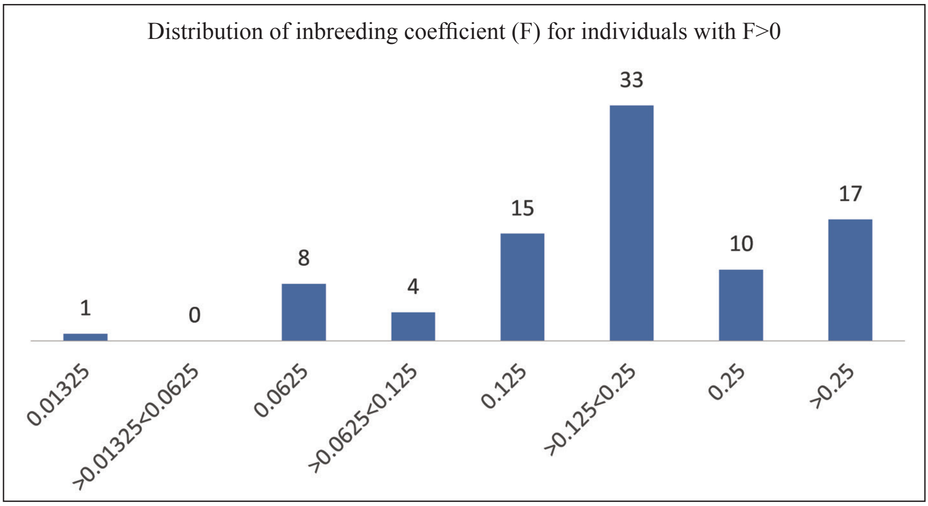

Figure 2 The distribution of inbreeding coefficients (F) for individuals with F>0. Most of the individuals have inbreeding events with close relatives (F≥0.125).

Table 2 Frequency of inbreeding events depending on dataset used: individuals with information of both parents and at least one grandparent (N1) or with all four grandparents known (N2).

Inbreeding Events	N1	% of inbred	N2	% of inbred
F=0	53	-	0	-
F=0.01325	1	0.71	1	1.15
0.01325<F<0.0625	0	0.00	0	0.00
F=0.0625	8	5.67	8	9.20
0.0625<F<0.125	4	2.84	4	4.60
F=0.125	15	10.64	15	17.24
0.125<F<0.25	33	23.40	33	37.93
F=0.25	10	7.09	9	10.34
F>0.25	17	12.06	17	19.54
Total F>0	88	62.41	87	100.00

Gaur calves were less likely to survive their first year with increasing inbreeding coefficient (Figure 3). For individuals born between 2000 and 2015, the first year survival rate is 100% when F=0. However, when F≥0.2500, only less than half survived their first year. The mortality rate is calculated to be 50.5% of which almost half of it was contributed by neonate mortality (did not survive the first 28 days of life). This result suggests that there is evidence of inbreeding depression in this captive gaur population.

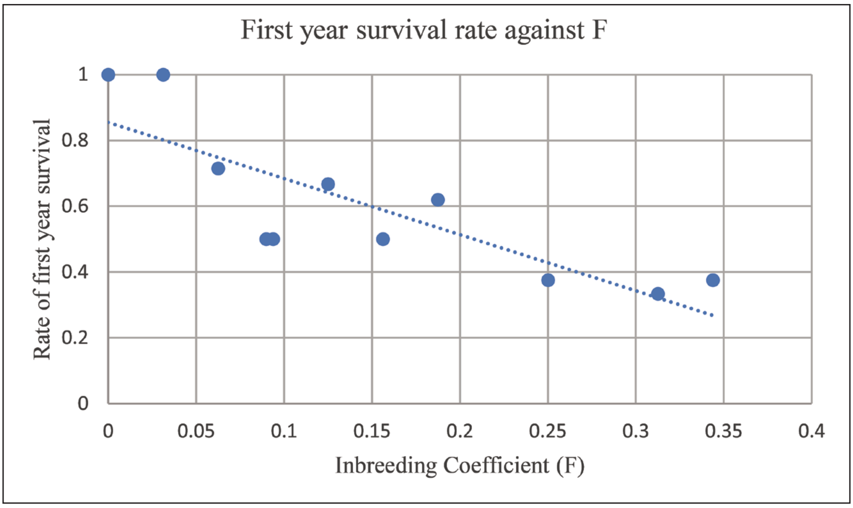

Figure 3 Relationship between offspring's inbreeding coefficient (F) and probability of first year survival.

This assessment has provided general idea on the current status of inbreeding at JSWCC but should be viewed as a preliminary assessment due to the small sample size. To get more insight into the inbreeding situation, it is crucial to study inbreeding at molecular level using genetic approach. According to Kardos et al. (2015), genetic approach can estimate inbreeding more precisely than pedigree data. In addition, introducing new bloodline into the captive population should become DWNP's top priority in order to maintain a high level of genetic variation and to ensure that the population in captive is viable for re-introduction into the wild.

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